

SEQUENCE LISTING

At
(1) GENERAL INFORMATION

- (i) APPLICANT: Motoharu SEIKI et al.
- (ii) TITLE OF INVENTION: NOVEL PROTEIN AND MONOCLONAL ANTIBODY SPECIFIC THERETO
- (iii) NUMBER OF SEQUENCES: 14
- (iv) CORRESPONDENCE ADDRESS:
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 - (C) CITY: Washington
 - (D) STATE: D.C.
 - (E) COUNTRY: U.S.A.
 - (F) ZIP: 20006
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: MS-DOS
 - (D) SOFTWARE: Wordperfect 5.1
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: NEW
 - (B) FILING DATE: December 12, 2000
 - (C) CLASSIFICATION:
- (vi) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 09/000,041
 - (B) FILING DATE: February 20, 1998
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: PCT/JP96/01956
 - (B) FILING DATE: July 12, 1996
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Lee Cheng
 - (B) REGISTRATION NUMBER: 40,949
 - (C) REFERENCE/DOCKET NUMBER:
- (ix) TELECOMMUNICATION INFORMATION:
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(2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2116
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GGCTCCTTAC CCACCCGGAG ACTTTTTTT GAAAGGAAAC TAGGGAGGGAGGGAGAGGGA	60
GAGAGGGAGA AACGAAAGGG GAGCTCGTCC ATCCATTGAA GCACAGTTCA CT ATG Met 1	115
ATC TTA CTC ACA TTC AGC ACT GGA AGA CGG TTG GAT TTC GTG CAT CAT Ile Leu Leu Thr Phe Ser Thr Gly Arg Arg Leu Asp Phe Val His His 5 10 15	163
TCG GGG GTG TTT TTC TTG CAA ACC TTG CTT TGG ATT TTA TGT GCT ACA Ser Gly Val Phe Phe Leu Gln Thr Leu Leu Trp Ile Leu Cys Ala Thr 20 25 30	211
GTC TGC GGA ACG GAG CAG TAT TTC AAT GTG GAG GTT TGG TTA CAA AAG Val Cys Gly Thr Glu Gln Tyr Phe Asn Val Glu Val Trp Leu Gln Lys 35 40 45	259
TAC GGC TAC CTT CCA CCG ACT GAC CCC AGA ATG TCA GTG CTG CGC TCT Tyr Gly Tyr Leu Pro Pro Thr Asp Pro Arg Met Ser Val Leu Arg Ser 50 55 60 65	307
GCA GAG ACC ATG CAG TCT GCC CTA GCT GCC ATG CAG CAG TTC TAT GGC Ala Glu Thr Met Gln Ser Ala Leu Ala Ala Met Gln Gln Phe Tyr Gly 70 75 80	355
ATT AAC ATG ACA GGA AAA GTG GAC AGA AAC ACA ATT GAC TGG ATG AAG Ile Asn Met Thr Gly Lys Val Asp Arg Asn Thr Ile Asp Trp Met Lys 85 90 95	403
AAG CCC CGA TGC GGT GTA CCT GAC CAG ACA AGA GGT AGC TCC AAA TTT Lys Pro Arg Cys Gly Val Pro Asp Gln Thr Arg Gly Ser Ser Lys Phe 100 105 110	451
CAT ATT CGT CGA AAG CGA TAT GCA TTG ACA GGA CAG AAA TGG CAG CAC His Ile Arg Arg Lys Arg Tyr Ala Leu Thr Gly Gln Lys Trp Gln His 115 120 125	499
AAG CAC ATC ACT TAC AGT ATA AAG AAC GTA ACT CCA AAA GTA GGA GAC Lys His Ile Thr Tyr Ser Ile Lys Asn Val Thr Pro Lys Val Gly Asp 130 135 140 145	547
CCT GAG ACT CGT AAA GCT ATT CGC CGT GCC TTT GAT GTG TGG CAG AAT Pro Glu Thr Arg Lys Ala Ile Arg Arg Ala Phe Asp Val Trp Gln Asn 150 155 160	595
GTA ACT CCT CTG ACA TTT GAA GAA GTT CCC TAC AGT GAA TTA GAA AAT Val Thr Pro Leu Thr Phe Glu Glu Val Pro Tyr Ser Glu Leu Glu Asn 165 170 175	643

GGC AAA CGT GAT GTG GAT ATA ACC ATT ATT TTT GCA TCT GGT TTC CAT Gly Lys Arg Asp Val Asp Ile Thr Ile Ile Phe Ala Ser Gly Phe His 180 185 190	691
GGG GAC AGC TCT CCC TTT GAT GGA GAG GGA GGA TTT TTG GCA CAT GCC Gly Asp Ser Ser Pro Phe Asp Gly Glu Gly Gly Phe Leu Ala His Ala 195 200 205	739
TAC TTC CCT GGA CCA GGA ATT GGA GGA GAT ACC CAT TTT GAC TCA GAT Tyr Phe Pro Gly Pro Gly Ile Gly Asp Thr His Phe Asp Ser Asp 210 215 220 225	787
GAG CCA TGG ACA CTA GGA AAT CCT AAT CAT GAT GGA AAT GAC TTA TTT Glu Pro Trp Thr Leu Gly Asn Pro Asn His Asp Gly Asn Asp Leu Phe 230 235 240	835
CTT GTA GCA GTC CAT GAA CTG GGA CAT GCT CTG GGA TTG GAG CAT TCC Leu Val Ala Val His Glu Leu Gly His Ala Leu Gly Leu Glu His Ser 245 250 255	883
AAT GAC CCC ACT GCC ATC ATG GCT CCA TTT TAC CAG TAC ATG GAA ACA Asn Asp Pro Thr Ala Ile Met Ala Pro Phe Tyr Gln Tyr Met Glu Thr 260 265 270	931
GAC AAC TTC AAA CTA CCT AAT GAT GAT TTA CAG GGC ATC CAG AAA ATA Asp Asn Phe Lys Leu Pro Asn Asp Asp Leu Gln Gly Ile Gln Lys Ile 275 280 285	979
TAT GGT CCA CCT GAC AAG ATT CCT CCA CCT ACA AGA CCT CTA CCG ACA Tyr Gly Pro Pro Asp Lys Ile Pro Pro Pro Thr Arg Pro Leu Pro Thr 290 295 300 305	1027
GTG CCC CCA CAC CGC TCT ATT CCT CCG GCT GAC CCA AGG AAA AAT GAC Val Pro Pro His Arg Ser Ile Pro Pro Ala Asp Pro Arg Lys Asn Asp 310 315 320	1075
AGG CCA AAA CCT CCT CGG CCT CCA ACC GGC AGA CCC TCC TAT CCC GGA Arg Pro Lys Pro Pro Arg Pro Pro Thr Gly Arg Pro Ser Tyr Pro Gly 325 330 335	1123
GCC AAA CCC AAC ATC TGT GAT GGG AAC TTT AAC ACT CTA GCT ATT CTT Ala Lys Pro Asn Ile Cys Asp Gly Asn Phe Asn Thr Leu Ala Ile Leu 340 345 350	1171
CGT CGT GAG ATG TTT GTT TTC AAG GAC CAG TGG TTT TGG CGA GTG AGA Arg Arg Glu Met Phe Val Phe Lys Asp Gln Trp Phe Trp Arg Val Arg 355 360 365	1219
AAC AAC AGG GTG ATG GAT GGA TAC CCA ATG CAA ATT ACT TAC TTC TGG Asn Asn Arg Val Met Asp Gly Tyr Pro Met Gln Ile Thr Tyr Phe Trp 370 375 380 385	1267
CGG GGC TTG CCT AGT ATC GAT GCA GTT TAT GAA AAT AGC GAC GGG Arg Gly Leu Pro Pro Ser Ile Asp Ala Val Tyr Glu Asn Ser Asp Gly 390 395 400	1315

AAT TTT GTG TTC TTT AAA GGT AAC AAA TAT TGG GTG TTC AAG GAT ACA Asn Phe Val Phe Phe Lys Gly Asn Lys Tyr Trp Val Phe Lys Asp Thr 405 410 415	1363
ACT CTT CAA CCT GGT TAC CCT CAT GAC TTG ATA ACC CTT GGA AGT GGA Thr Leu Gln Pro Gly Tyr Pro His Asp Leu Ile Thr Leu Gly Ser Gly 420 425 430	1411
ATT CCC CCT CAT GGT ATT GAT TCA GCC ATT TGG TGG GAG GAC GTC GGG Ile Pro Pro His Gly Ile Asp Ser Ala Ile Trp Trp Glu Asp Val Gly 435 440 445	1459
AAA ACC TAT TTC TTC AAG GGA GAC AGA TAT TGG AGA TAT AGT GAA GAA Lys Thr Tyr Phe Phe Lys Gly Asp Arg Tyr Trp Arg Tyr Ser Glu Glu 450 455 460 465	1507
ATG AAA ACA ATG GAC CCT GGC TAT CCC AAG CCA ATC ACA GTC TGG AAA Met Lys Thr Met Asp Pro Gly Tyr Pro Lys Pro Ile Thr Val Trp Lys 470 475 480	1555
GGG ATC CCT GAA TCT CCT CAG GGA GCA TTT GTA CAC AAA GAA AAT GGC Gly Ile Pro Glu Ser Pro Gln Gly Ala Phe Val His Lys Glu Asn Gly 485 490 495	1603
TTT ACG TAT TTC TAC AAA GGA AAG GAG TAT TGG AAA TTC AAC AAC CAG Phe Thr Tyr Phe Tyr Lys Gly Lys Glu Tyr Trp Lys Phe Asn Asn Gln 500 505 510	1651
ATA CTC AAG GTA GAA CCT GGA CAT CCA AGA TCC ATC CTC AAG GAT TTT Ile Leu Lys Val Glu Pro Gly His Pro Arg Ser Ile Leu Lys Asp Phe 515 520 525	1699
ATG GGC TGT GAT GGA CCA ACA GAC AGA GTT AAA GAA GGA CAC AGC CCA Met Gly Cys Asp Gly Pro Thr Asp Arg Val Lys Glu Gly His Ser Pro 530 535 540 545	1747
CCA GAT GAT GTA GAC ATT GTC ATC AAA CTG GAC AAC ACA GCC AGC ACT Pro Asp Asp Val Asp Ile Val Ile Lys Leu Asp Asn Thr Ala Ser Thr 550 555 560	1795
GTG AAA GCC ATA GCT ATT GTC ATT CCC TGC ATC TTG GCC TTA TGC CTC Val Lys Ala Ile Ala Ile Val Ile Pro Cys Ile Leu Ala Leu Cys Leu 565 570 575	1843
CTT GTA TTG GTT TAC ACT GTG TTC CAG TTC AAG AGG AAA GGA ACA CCC Leu Val Leu Val Tyr Thr Val Phe Gln Phe Lys Arg Lys Gly Thr Pro 580 585 590	1891
CGC CAC ATA CTG TAC TGT AAA CGC TCT ATG CAA GAG TGG GTG TGATGTAGG Arg His Ile Leu Tyr Cys Lys Arg Ser Met Gln Glu Trp Val 595 600 605	1942
GTTTTTCTT CTTTCTTCTT TTTGCAGGAG TTTGTGGTAA CTTGAGATTC AAGACAAGAG	2002
CTGTTATGCT GTTCTCTAGC TAGGAGCAGG CTTGTGGCAG CCTGATTCTGG GGCTGACCTT	2062
TCAAACCAGA GGGTTGCTGG TCCTGCACAT GAGTGGAAAT ACACTCATGG GGAA	2116

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 607
 (B) TYPE: Amino acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met	Ile	Leu	Leu	Thr	Phe	Ser	Thr	Gly	Arg	Arg	Leu	Asp	Phe	Val	His
1					5				10					15	
His	Ser	Gly	Val	Phe	Phe	Leu	Gln	Thr	Leu	Leu	Trp	Ile	Leu	Cys	Ala
						20			25				30		
Thr	Val	Cys	Gly	Thr	Glu	Gln	Tyr	Phe	Asn	Val	Glu	Val	Trp	Leu	Gln
		35			40						45				
Lys	Tyr	Gly	Tyr	Leu	Pro	Pro	Thr	Asp	Pro	Arg	Met	Ser	Val	Leu	Arg
					50				55		60				
Ser	Ala	Glu	Thr	Met	Gln	Ser	Ala	Leu	Ala	Ala	Met	Gln	Gln	Phe	Tyr
				65				70		75				80	
Gly	Ile	Asn	Met	Thr	Gly	Lys	Val	Asp	Arg	Asn	Thr	Ile	Asp	Trp	Met
					85				90				95		
Lys	Lys	Pro	Arg	Cys	Gly	Val	Pro	Asp	Gln	Thr	Arg	Gly	Ser	Ser	Lys
					100				105				110		
Phe	His	Ile	Arg	Arg	Lys	Arg	Tyr	Ala	Leu	Thr	Gly	Gln	Lys	Trp	Gln
					115				120				125		
His	Lys	His	Ile	Thr	Tyr	Ser	Ile	Lys	Asn	Val	Thr	Pro	Lys	Val	Gly
						130			135				140		
Asp	Pro	Glu	Thr	Arg	Lys	Ala	Ile	Arg	Arg	Ala	Phe	Asp	Val	Trp	Gln
					145				150				155		160
Asn	Val	Thr	Pro	Leu	Thr	Phe	Glu	Glu	Val	Pro	Tyr	Ser	Glu	Leu	Glu
					165				170				175		
Asn	Gly	Lys	Arg	Asp	Val	Asp	Ile	Thr	Ile	Ile	Phe	Ala	Ser	Gly	Phe
					180				185				190		
His	Gly	Asp	Ser	Ser	Pro	Phe	Asp	Gly	Glu	Gly	Gly	Phe	Leu	Ala	His
					195				200				205		
Ala	Tyr	Phe	Pro	Gly	Pro	Gly	Ile	Gly	Gly	Asp	Thr	His	Phe	Asp	Ser

210	215	220
Asp Glu Pro Trp Thr Leu Gly Asn Pro Asn His Asp Gly Asn Asp Leu		
225	230	235
240		
Phe Leu Val Ala Val His Glu Leu Gly His Ala Leu Gly Leu Glu His		
245	250	255
Ser Asn Asp Pro Thr Ala Ile Met Ala Pro Phe Tyr Gln Tyr Met Glu		
260	265	270
Thr Asp Asn Phe Lys Leu Pro Asn Asp Asp Leu Gln Gly Ile Gln Lys		
275	280	285
Ile Tyr Gly Pro Pro Asp Lys Ile Pro Pro Pro Thr Arg Pro Leu Pro		
290	295	300
Thr Val Pro Pro His Arg Ser Ile Pro Pro Ala Asp Pro Arg Lys Asn		
305	310	315
320		
Asp Arg Pro Lys Pro Pro Arg Pro Pro Thr Gly Arg Pro Ser Tyr Pro		
325	330	335
Gly Ala Lys Pro Asn Ile Cys Asp Gly Asn Phe Asn Thr Leu Ala Ile		
340	345	350
Leu Arg Arg Glu Met Phe Val Phe Lys Asp Gln Trp Phe Trp Arg Val		
355	360	365
Arg Asn Asn Arg Val Met Asp Gly Tyr Pro Met Gln Ile Thr Tyr Phe		
370	375	380
Trp Arg Gly Leu Pro Pro Ser Ile Asp Ala Val Tyr Glu Asn Ser Asp		
375	390	395
400		
Gly Asn Phe Val Phe Phe Lys Gly Asn Lys Tyr Trp Val Phe Lys Asp		
405	410	415
Thr Thr Leu Gln Pro Gly Tyr Pro His Asp Leu Ile Thr Leu Gly Ser		
420	425	430
Gly Ile Pro Pro His Gly Ile Asp Ser Ala Ile Trp Trp Glu Asp Val		
435	440	445
Gly Lys Thr Tyr Phe Phe Lys Gly Asp Arg Tyr Trp Arg Tyr Ser Glu		
450	455	460
460		
Glu Met Lys Thr Met Asp Pro Gly Tyr Pro Lys Pro Ile Thr Val Trp		
465	470	475
480		
Lys Gly Ile Pro Glu Ser Pro Gln Gly Ala Phe Val His Lys Glu Asn		
485	490	495
Gly Phe Thr Tyr Phe Tyr Lys Gly Lys Glu Tyr Trp Lys Phe Asn Asn		
500	505	510
Gln Ile Leu Lys Val Glu Pro Gly His Pro Arg Ser Ile Leu Lys Asp		

515	520	525
Phe Met Gly Cys Asp Gly Pro Thr Asp Arg Val Lys Glu Gly His Ser		
530	535	540
Pro Pro Asp Asp Val Asp Ile Val Ile Lys Leu Asp Asn Thr Ala Ser		
545	550	555
Thr Val Lys Ala Ile Ala Ile Val Ile Pro Cys Ile Leu Ala Leu Cys		
565	570	575
Leu Leu Val Leu Val Tyr Thr Val Phe Gln Phe Lys Arg Lys Gly Thr		
580	585	590
Pro Arg His Ile Leu Tyr Cys Lys Arg Ser Met Gln Glu Trp Val		
595	600	605

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Other nucleic acid
Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

SGNVVNGCWG AYATMRTSAT 20

(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Other nucleic acid
Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

YTCRTSNTCR TCRAARTGRR HRTCYCC 27

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14
 - (B) TYPE: Amino acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Gln Thr Arg Gly Ser Ser Lys Phe His Ile Arg Arg Lys Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14
- (B) TYPE: Amino acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Glu Glu Val Pro Tyr Ser Glu Leu Glu Asn Gly Lys Arg Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18
- (B) TYPE: Amino acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Pro Thr Ser Pro Arg Met Ser Val Val Arg Ser Ala Glu Thr Met Gln
1 5 10 15

Ser Ala

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14
- (B) TYPE: Amino acid
- (D) STRANDEDNESS: Single
- (C) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Thr Leu Gly Asn Pro Asn His Asp Gly Asn Asp Leu Phe Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 9:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 7
(B) TYPE: Amino acid
(D) STRANDEDNESS: Single
(C) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

Gly Glu Ala Asp Ile Leu Val
1 5

(2) INFORMATION FOR SEQ ID NO: 10:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 9
(B) TYPE: Amino acid
(D) STRANDEDNESS: Single
(C) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Gly Asp Ala His Phe Asp Asp Asp Glu
1 5

(2) INFORMATION FOR SEQ ID NO: 11:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 7
(B) TYPE: Amino acid
(D) STRANDEDNESS: Single
(C) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

Gly Glu Ala Asp Ile Met Ile
1 5

(2) INFORMATION FOR SEQ ID NO: 12:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 7
(B) TYPE: Amino acid
(D) STRANDEDNESS: Single
(C) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Pro Arg Cys Gly Val Pro Asp
1 5

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

Ala Ile Ala Ile Val Ile Pro Cys Ile Leu Ala Leu Cys Leu Leu
1 5 10 15

Val Leu Val Tyr Thr Val Phe Gln Phe
20

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Arg Xaa Lys Arg
1